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Evaluation of Genetic Variation in Indian mustard (*Brassica Juncea* L Czern and Coss) Using Multivariate Techniques

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Abstract

A set of 310 lines of Indian mustard (*Brassica juncea* L Czern and Coss) were analysed for cluster and principal component analysis (PCA). PCA identified four principal components which explained 65.13% of total variability among the 310 genotypes. Hierarchical cluster analysis grouped 310 genotypes into 3 clusters. Cluster1 included maximum number of 155 genotypes and clusters 3 had the lowest number of 43 genotypes. The grouping pattern of genotypes obtained by cluster analysis and PCA plots was almost similar.

Key words : Indian mustard genotypes, cluster analysis, principal component analysis.

Indian mustard (*Brassica juncea* L. Czern and Coss.) is the most important crop among the rapeseed-mustard grown in India. India is the fourth largest oilseed economy in the world. Among the seven oilseeds cultivated in India, rapeseed-mustard contributes 28.6% in the total oilseeds production Mustard seed is the second most important oil seed crop in India after soyabean. Haryana accounts for 11 per cent of the total area and 16 per cent of the total production in the country. Indian mustard accounts for nearly 21% of the total oilseeds produced in the country (http://www.religareonline.com /research/Disclaimer/Disclaimer_rcl.html) [1]. Total production of rapeseed mustard in India for the year 2013-14 was 72.82 lakh tonnes, which has increased by 9.5% as compared to previous year.

To boost up the productivity of Indian mustard, hybridization and exploitation of heterosis may play significant role. For developing better genotypes/hybrids, the choice of suitable parents is a matter of great concern to the plant breeders. For this purpose, breeders conduct experiments and record data on a number of variables. So, in general, breeders are to select the best genotypes by discarding those least useful for the final decision making and maintaining high performance.

Hamman (1972)[2] suggested that the use of multivariate techniques could reduce several phenotypic measurements in large populations into fewer, more interpretable, and easily visualized dimensions. Several other researchers have worked on similar lines regarding selection of diverse genotypes for breeding purpose. Acharya and Swain (2003)[3] have worked on genetic divergence in Indian mustard. Shathi *et al*. (2012) [4] conducted field experiment of 25 mustard (Brassica spp. L) genotypes with eleven quantitative characteristics to study the genetic diversity. Cluster analysis was used for grouping the 25 mustards (Brassica sp. L) genotypes into six clusters. Neeru *et al*. (2015)[5] used principal component analysis and hierarchical cluster analysis on 25 characters in 60 genotypes of Indian mustard (*Brassica juncea* L.) identified 11 principal components which explained about 75% variability. Using cluster analysis all the 60

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genotypes were categorized into 10 clusters. The results of cluster and principal factor analysis confirmed each other. Chaudhary *et al.* (2015)[6] analysed a set of 66 lines of pearl millet using cluster and principal component analysis. PCA identified six principal components which explained 77.7% of total variability among the 66 genotypes. Hierarchical cluster analysis grouped 66 genotypes into six clusters. The grouping pattern of genotypes obtained by cluster analysis and PCA plots was almost similar.

The multivariate analysis is an important tool for assessment of genetic divergence of the genotypes. Various first degree and second degree statistics are available for grouping of the genotypes to select for diverse types, but sometimes the recorded data become unmanageable and complicated to interpret. Often PCA and cluster analysis have been used to reduce large no of genotypes upto manageable level to identify the characters of significance to be used in a fresh breeding programme with a greater degree of reliance.

The present investigation was undertaken on 310 genotypes of Indian mustard for evaluation and grouping for similarity and degree of genetic diversity based on data recorded on 11 characters using PCA and cluster analysis.

Materials and Methods

In the present study, secondary data on Indian mustard genotypes was obtained from experiment conducted by the Oilseeds section of the department of Genetics and Plant Breeding, CCSHAU, Hisar. Data were recorded on 310 genotypes on 11 characters *viz*., plant height, 1000 seed wt, siliqua length, main shoot length, siliqua no, seed yield, days of maturity, oil content, primary branches, secondry branches, seeds/siliqua. Statistical tools like cluster analysis (CA) and principal component analysis (PCA) were used for groupig of genotypes into similar groups based on their agronomic traits and seed yield. Cluster analysis was performed using Ward's hierarchical clustering algorithm.

Methods

Principal Component Analysis : Principal component analysis is a statistical tool for data exploration and feature extraction in multivariate analysis. The procedure consists of finding the eigen roots and eigen vectors of the correlation matrix of explanatory variables. Interpretation of principal components is often facilitated by computing the components loadings. PC loadings are correlation coefficients between the PC scores and the original variables. PC loadings measure the importance of each variable in accounting for the variability in the PC. One of the most commonly used criteria for solving the number of components problem is the eigen value, also known as the Kaiser's (1960)[7] criterion.

Cluster Analysis : Cluster analysis is also one of the methods of data reduction technique. PCA reduces the number of variables whereas cluster analysis reduces the number of observations. Cluster analysis identifies homogeneous groups or clusters. It helps in grouping the materials in such a manner that similar types are grouped together while dissimilar ones belong to different groups.

Results and Discussion

Correlation matrix based principal component analysis was performed to extract the principal dimensions for agronomic traits and seed yield. The variance of each component and the percentage of cumulative variation explained by various principal components are presented in Table 1. Four PCs with eigen values greater than one were retained (Jeffers, 1967)[8].

Table 1. Total variance explained by various principal components

Components	PC1	PC2	PC3	PC4	PC5	PC6	PC7	PC8	PC9	PC10	PC11
Eigenvalue	2.66	1.89	1.52	1.10	0.99	0.89	0.61	0.53	0.40	0.21	0.20
Variability%	24.16	17.21	13.80	9.96	9.00	8.11	5.54	4.82	3.62	1.93	1.86
Cumulative%	24.16	41.37	55.17	65.13	74.13	82.24	87.78	92.60	96.22	98.14	100.00

The first four principal components were with eigen values more than one together explained 65.13% of the total variability. Only siliqua no. contributed positively to all the four PCs. The component loadings for the characters secondary branches, 1000 seed wt, siliqua length, primary branches contributed the maximum to the first principal component which accounted for 24.16% variation indicating that the Indian mustard genotypes were differentiated on the basis of these characters. Main shoot length and siliqua no. were the characters contributing to the second principal component, accounted for 17.21% of the total variability. The character seed yield and Days of maturity contributed to the third principal component which explained 13.80% variation. The fourth principal component accounting for 9.96% variability had high loading for the character seed siliqua. The character days of maturity had high loading for PC3 and PC4 while seed yield for PC1 and PC3.

The analysis without rotation of axes failed to load all the variables signifying that it could not offer much information regarding the idea of correlation between the variables and the principal components. The Varimax rotation thus, applied resulted in loading of all the variables on different principal components. Factor loading of different variables obtained through varimax rotation are presented in Table 2. All the 11 variables showed high loading on different PCs and none of them was left rotation of the factor axes. Moreover, it already grouped the similar type of variables by loading them together as a common PC. The principal components 1, 2 and 4 assigned for 5 variables secondary branches, 1000 seed wt, siliqua length, primary branches and seeds/siliqua in total related to yield can be designated as yield factor. The principal component 2 and 3 showing high loadings for main shoot length and seed yield are related to the growth rate at different stages and vegetative parameters. These together can be designated as growth rate. Such a clear grouping of similar type of variables having loaded on a common principal component elaborates the successful transformation of eleven interrelated variables into four independent principal components explaining 65.13% of the variability of the original set.

Two main components have been extracted having eigen value more than one. They account for 41.37% of the total variability. The first main component (PC1) explaining 24.16% of total variation and was positively correlated

Table 2. Loadings of different characters with respect to different PC's

Characters	Principal Components			
	1	2	3	4
Secondry branches	*0.787	-0.281	0.173	0.127
1000 seed wt	*-0.711	0.186	0.460	-0.093
Siliqua length	*-0.695	-0.073	0.470	0.214
Primary branches	*0.640	-0.304	0.093	0.170
Plant height	0.436	0.373	0.219	-0.363
Main shoot length	-0.007	*0.842	0.215	0.346
Siliqua no.	0.483	*0.757	0.078	0.243
Seed yield	0.420	-0.176	*0.686	0.179
Days of maturity	0.121	-0.145	*0.637	-0.551
Oil content	0.087	0.067	-0.217	-0.151
Seeds/siliqua	-0.136	-0.451	0.151	*0.572

with plant height, days to maturity, primary branches, secondary branches and seeds/siliqua whereas it was negatively correlated with siliqua no. main shoot length, 1000 seed wt, oil content and siliqua length (Fig. 1). This implies that, genotypes with high values of PC1 have lower oil content and vice versa. The second main component (PC2) accounted 17.21% of the total variation and was negatively associated with seed/siliqua, primary branches, secondary branches while positively associated with remaining characters (Fig. 1). This means that, genotypes with high values of PC2 have lower 1000 seed wt, siliqua length, plant height, main shoot length, siliqua no., seed yield, days of maturity, oil content. In this condition selecting the genotypes for higher yield is easy because in both main components positive coefficients with seed yield were obtained.

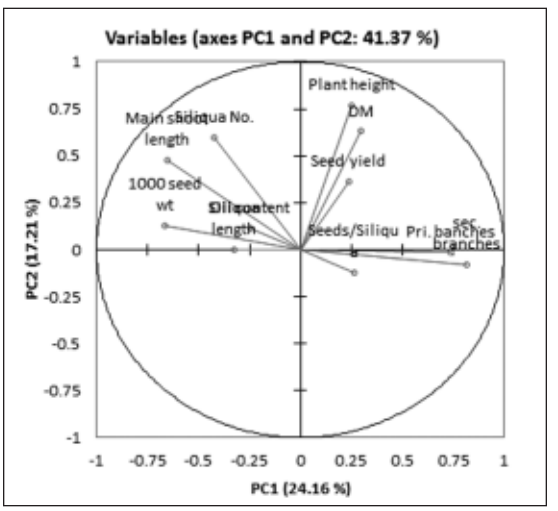

Fig. 1. Correlation between PC1 and PC2

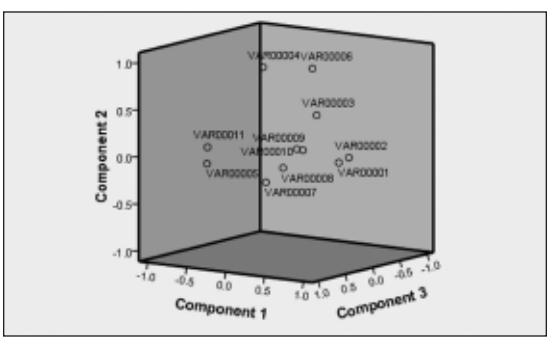

Fig. 2. 3D plot for first three principal component scores

Cluster analysis is an important statistical technique for the study of genetic diversity among genotypes which is of great practical significance for the plant breeders (Chaudhary *et al*., 2015)[6]. Cluster analysis using ward's method based on quantitative traits, all mustard genotypes were grouped into three clusters. Out of total 310 genotypes, the maximum of 155 genotypes formed cluster I. In second cluster there were 112 genotypes and third cluster contained 43 genotypes. To assess the diversity, inter and intra cluster distances were calculated and are presented in Table 3. The maximum inter cluster distance (52.018) was noted between cluster I and III, followed by (26.442) between cluster II and III, (25.759) between clusters I and II indicating that the lines grouped in these clusters were diverse and selected lines could be intercrossed to prepare a base population to combine the desirable characteristics. The clustering pattern further shows different genotypes were grouped in same cluster, this shows geographical diversity could not necessarily be an index of genetic variability, and the factors other than geographic diversity such as selection pressure and environment may be responsible for differential grouping of genotypes. The groupings obtained in 3-D plot of principal components (Figure 2) demonstrating the distribution in the first three principal components clearly showed the separation of 310 genotypes evaluated into four different groups. The results of PCA were closely in accordance with those of the cluster analysis.

Table 3. Average Inter and intra-cluster distances

Cluster No	I	II	III
I	0	25.759	52.018
II	25.759	0	26.442
III	52.018	26.442	0

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Role of Molecular Motors in Endosomal Dynamics: A review

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Abstract

Molecular motors are continually agitated by random Brownian motion, which provides both challenges and opportunities for energy conversion mechanisms. Molecular motors, an important class of molecular machines, harness various energy sources to generate unidirectional mechanical motion. In biological systems, molecular motors made of proteins and nucleic acids are ubiquitous, and commonly use the chemical energy of ATP or the electrochemical potential of protons across the cell membrane (the so-called proton-motive force) as an energy source. ATP synthase and V-ATPase also act as energy converters, in which ATP chemical energy and proton electrochemical potential are reversibly converted via mechanical rotation. In the cytoplasm of eukaryotic cells, three different classes of motors that generate linear movement are known to exist – myosin, kinesin and dynein. Most motors studied so far in some detail can generate a force that is sufficient to move even large objects through viscous cytoplasm.

Key words : ATP, brownian, dynein, kinesin, molecular motors, myosin.

Molecular motors are enzymes that transform chemical energy into mechanical work. Cytoskeletal motor proteins that move unidirectionally along an oriented polymer track either towards the plus end or the minus end of the track. These have the ability to use chemical energy to propel them along a linear track, with the direction of sliding dependent on the structural polarity of the track. All of them generate motion by coupling nucleoside

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